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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/086,623

DATE: 03/14/2002 P.5
TIME: 12:27:56

Input Set : A:\10086623.txt
Output Set: N:\CRF3\03142002\J086623.raw

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       4 <110> APPLICANT: ERIKSSON, Ulf
       5         AASE, Karin
       6         LI, Xuri
       7         PONTEN, Annica
       8         UUTELA, Marko
       9         ALITALO, Kari
      10         OESTMAN, Arne
      11         HELDIN, Carl-Henrik
      13 <120> TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND
USES THEREOF
      16 <130> FILE REFERENCE: 1064/44833C2
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/086,623
C--> 19 <141> CURRENT FILING DATE: 2000-03-04
      19 <150> PRIOR APPLICATION NUMBER: US 60/107,852
      20 <151> PRIOR FILING DATE: 1998-11-10
      23 <150> PRIOR APPLICATION NUMBER: US 60/113,997
      24 <151> PRIOR FILING DATE: 1998-12-28
      27 <150> PRIOR APPLICATION NUMBER: US 60/150,604
      28 <151> PRIOR FILING DATE: 1999-08-26
      31 <150> PRIOR APPLICATION NUMBER: US 60/157,108
      32 <151> PRIOR FILING DATE: 1999-10-04
      35 <150> PRIOR APPLICATION NUMBER: US 60/157,756
      36 <151> PRIOR FILING DATE: 1999-10-05
      39 <150> PRIOR APPLICATION NUMBER: US 09/438,046
      40 <151> PRIOR FILING DATE: 1999-11-10
      43 <150> PRIOR APPLICATION NUMBER: US 09/691,200
      44 <151> PRIOR FILING DATE: 2000-10-19
      47 <160> NUMBER OF SEQ ID NOS: 42
      50 <170> SOFTWARE: PatentIn version 3.1
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      55 <211> LENGTH: 360
      57 <212> TYPE: DNA
      59 <213> ORGANISM: Homo sapiens
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      66 aaaaagtatc atgaggtatt acagtttgag cctggccaca tcaagaggag gggtagagct      120
      68 aagaccatgg ctctagttga catccagttg gatcaccatg aacgatgtga ttgtatctgc      180
      70 agctcaagac cacctcgata agagaatgtg cacatcctta cattaagcct gaaagaacca      240
      72 ttagtttaag gagggtgaga taagagaccc ttttcctacc agcaaccaga cttactacta      300
      74 gcctgcaatg caatgaacac aagtggttgc tgagtctcag ccttgctttg ttaatgccat      360
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      79 <211> LENGTH: 66
      81 <212> TYPE: PRT
      83 <213> ORGANISM: Homo sapiens
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Input Set : A:\10086623.txt
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87 <400> SEQUENCE: 2
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93 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
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97 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
98   35   40   45
101 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
102   50   55   60
105 Pro Arg
106 65
109 <210> SEQ ID NO: 3
111 <211> LENGTH: 690
113 <212> TYPE: DNA
115 <213> ORGANISM: Homo sapiens
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122 tcagggtatc cctataactc tccatcagta acggatccca ctctgattgc ggatgctctg   120
124 gacaaaaaaa ttgcagaatt tgatacagtg gaagatctgc tcaagtactt caatccagag   180
126 tcatggcaag aagatcttga gaatatgtat ctggacaccc ctcggtatcg aggcaggtca   240
128 taccatgacc ggaagtcaaa agttgacctg gataggctca atgatgatgc caagcgttac   300
130 agttgcactc ccaggaatta ctcggtcaat ataagagaag agctgaagtt ggccaatgtg   360
132 gtcttctttc cacgttgcct cctcgtgcag cgctgtggag gaaattgtgg ctgtggaact   420
134 gtcaaactgg agtcctgcac atgcaattca gggaaaaccg tgaaaaagta tcatgaggta   480
136 ttacagtttg agcctggcca catcaagagg aggggtagag ctaagaccat ggctctagtt   540
138 gacatccagt tggatcacca tgaacgatgc gattgtatct gcagctcaag accacctcga   600
140 taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta aggagggtga   660
142 gataagagac ccttttccta ccagcaaccc   690
145 <210> SEQ ID NO: 4
147 <211> LENGTH: 200
149 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
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161 Thr Ser Ser Val Ser Gly Tyr Pro Tyr Asn Ser Pro Ser Val Thr Asp
162   20   25   30
165 Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp
166   35   40   45
169 Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu
170   50   55   60
173 Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser
174 65   70   75   80
177 Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp
178   85   90   95
181 Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg
182   100   105   110
185 Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu
186   115   120   125

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189 Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu
190     130                 135                 140
193 Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val
194 145                 150                 155                 160
197 Leu Gln Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr
198                 165                 170                 175
201 Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys
202                 180                 185                 190
205 Ile Cys Ser Ser Arg Pro Pro Arg
206             195                 200
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211 <211> LENGTH: 1934
213 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
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221 <221> NAME/KEY: CDS
223 <222> LOCATION: (1)..(966)
225 <223> OTHER INFORMATION:
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230 ttg tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg     48
231 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
232 1               5                   10                  15
234 cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca     96
235 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
236             20                  25                  30
238 tgg cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac    144
239 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
240         35                  40                  45
242 aat cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat    192
243 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
244     50                  55                  60
246 ttt gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga    240
247 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
248 65                  70                  75                  80
250 cga tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg    288
251 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
252             85                  90                  95
254 aac caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa    336
255 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
256             100                 105                 110
258 cct gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca    384
259 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
260         115                 120                 125
262 gca gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg    432
263 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
264     130                 135                 140
266 gta tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat    480
267 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
268 145                 150                 155                 160
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270 gct ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc    528
271 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
272             165             170             175
274 aag tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat    576
275 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
276             180             185             190
278 ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca    624
279 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
280             195             200             205
282 aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc    672
283 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
284     210             ·   215             220
286 act ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc    720
287 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
288 225             230             235             240
290 aat gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga    768
291 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
292             245             250             255
294 aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca    816
295 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
296             260             265             270
298 ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc    864
299 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
300             275             280             285
302 cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc    912
303 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
304     290             295             300
306 cag ttg gat cac cat gaa cga tgc gat tgt atc tgc agc tca aga cca    960
307 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
308 305             310             315             320
310 cct cga taagagaatg tgcacatcct tacattaagc ctgaagaac ctttagttta    1016
311 Pro Arg
314 aggagggtga gataagagac ccttttccta ccagcaacca aacttactac tagcctgcaa   1076
316 tgcaatgaac acaagtggtt gctgagtctc agccttgctt tgttaatgcc atggcaagta   1136
318 gaaaggtata tcatcaactt ctatacctaa gaatatagga ttgcatttaa taatagtgtt   1196
320 tgaggttata tatgcacaaa cacacacaga aatatattca tgtctatgtg tatatagatc   1256
322 aaatgttttt tttggtatat ataaccaggt acaccagagc ttacatatgt ttgagttaga   1316
324 ctcttaaaat cctttgccaa aataagggat ggtcaaatat atgaaacatg tctttagaaa   1376
326 atttaggaga taaatttatt tttaaatttt gaaacacaaa acaattttga atcttgctct   1436
328 cttaaagaaa gcatcttgta tattaaaaat caaaagatga ggctttctta catatacatc   1496
330 ttagttgatt attaaaaaag gaaaaaggtt tccagagaaa aggccaatac ctaagcattt   1556
332 tttccatgag aagcactgca tacttaccta tgtggactgt ataacctgt ctccaaaacc    1616
334 atgccataat aatataagtg ctttagaaat taaatcattg tgttttttat gcattttgct   1676
336 gaggcatcct tattcattta acacctatct caaaaactta cttagaaggt ttttttattat  1736
338 agtcctacaa aagacaatgt ataagctgta acagaatttt gaattgtttt tctttgcaaa   1796
340 acccctccac aaaagcaaat cctttcaaga atggcatggg cattctgtat gaacctttcc   1856
342 agatggtgtt cagtgaaaga tgtgggtagt tgagaactta aaaagtgaac attgaaacat   1916
344 cgacgtaact ggaaaccg                                                 1934
347 <210> SEQ ID NO: 6
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Input Set : A:\10086623.txt
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349 <211> LENGTH: 322
351 <212> TYPE: PRT
353 <213> ORGANISM: Homo sapiens
357 <400> SEQUENCE: 6
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363 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
364   20   25.   30
367 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
368   35   40   45
371 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
372   50   55   60
375 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
376 65   70   75   80
379 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
380   85   90   95
383 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
384   100   105   110
387 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
388   115   120 .   125
391 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
392   130   135   140
395 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
396 145   150   155   160
399 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
400   165   170   175
403 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
404   180   185   190
407 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
408   195   200   205
411 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
412   210   215   220
415 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
416 225   230   235   240
419 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
420   245   250   255
423 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
424   260   265   270
427 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
428   275   280   285
431 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
432   290   295   300
435 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
436 305   310   315   320
439 Pro Arg
443 <210> SEQ ID NO: 7
445 <211> LENGTH: 2253
447 <212> TYPE: DNA
449 <213> ORGANISM: Homo sapiens

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/086,623

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Input Set : **A:\10086623.txt**
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L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2205 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
L:2206 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
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